

1 : NM_000787 . Homo sapiens
 dopam...[gi:4503260]

PubMed, Protein, Related Sequences.
LinkOut

LOCUS NM_000787 2725 bp mRNA PRI 19-MAR-1999
 DEFINITION Homo sapiens dopamine beta-hydroxylase (dopamine
 beta-monooxygenase) (DBH) mRNA.
 ACCESSION NM_000787
 VERSION NM_000787.1 GI:4503260
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2725)
 AUTHORS Kobayashi,K., Kurosawa,Y., Fujita,K. and Nagatsu,T.
 TITLE Human dopamine beta-hydroxylase gene: two mRNA types having
 different 3'-terminal regions are produced through alternative
 polyadenylation
 JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
 MEDLINE 89160241
 REFERENCE 2 (bases 1 to 2725)
 AUTHORS Nagatsu,T.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry,
 Nagoya University, School of Medicine, Nagoya 466, Japan
 COMMENT REFSEQ: This reference sequence was derived from X13255.
 see also X13256 for type b mRNA
 Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50(1988).
 PROVISIONAL RefSeq: This is a provisional reference sequence
 record
 that has not yet been subject to human review. The final curated
 reference sequence record may be somewhat different from this one.
 FEATURES
 Location/Qualifiers
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 SDQKGQIHLDPPQDYQLLQVQRTPEGLTLLFKRPFGTCDPKDYLIEDGTVHLVYGILE

Figure 1A

EPFRSLEAINGSLQMGLQRVQLLKPNIPPELPDSDACTMEVQAPNIQIPSQETTYWC
YIKELPKGFSRHHIIKYEPIVTKGNEALVHHMEVFQCAPEMDSVPHFSGPCDSKMKPD
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IRLYYTAKLRRFNAGIMELGLVYTPVMAIPPRETAFILTYCTDKCTQLALPPSGIHI
FASQLHHTLTGRKVVTVLVRDGREWEIVNQDNHYSHPHFQEIRMLKKVVSVHPGDVLIT
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sig peptide 33..107
mat peptide 108..1841
/product="dopamine beta-hydroxylase (dopamine
beta-monooxygenase) "

BASE COUNT	533 a	901 c	774 g	517 t
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181	atgtcagcta	caccagagg	gccatccatt	tccagctcct
241	gcgtcctgtt	tgggatgtcc	gaccgtggcg	agcttgagaa
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1441	tggaggagat	gtgtgtcaac	tacgtgcact	actaccccca
1501	agacggctgt	ggacgccggc	ttcctgcaga	agtacttcca
1561	acgaggatgt	ctgcacctgc	cctcaggcgt	ccgtgtctca
1621	ggaactcctt	caaccgcgac	gtactgaagg	ccctgtacag
1681	actgcaacaa	gtcctcagcc	gtccgcttcc	aggtggaatg
1741	aggtcatctc	cacactggaa	gagccaccc	cacagtgcct

Figure 1B

1801 ctgctggccc caccgttgct agcattggtg ggggcaaagg ctgagggggg acctactcct
1861 cccctctctc catgctgtcc ctgtgggctc acaccggcac tgtgcactct actctgcgac
1921 gatcccatg gaacagccct gcacgccag gatgaagggg ccagaccacg cccctgctg
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2581 gctgtgcttt ccgctgggt ctgccactta gggagtgtgc cttggcggg ccatttcaca
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2701 caataaagct cacacttggg ctggc

Figure 1C

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SUMMARY OF DBH ASSOCIATION

Original study	Transmitted	Untransmitted	Chi-sq	p-val
DBHu2	28	21	0.53	0.4658
DBHu1	18	12	1.20	0.2733
DBHp444a	56	41	2.32	0.1278
Replication/DePaulo				
DBHu2	14	8	1.64	0.2008
DBHu1	11	13	0.17	0.6831
DBHp444a	49	38	1.39	0.2383
Totals				
DBHu2	40	29	1.75	0.1854
DBHu1	29	25	0.30	0.5852
DBHp444a	105	79	3.67	0.0553

DBH HAPLOTYPE ANALYSIS

Original Study	Transmitted	Untransmitted	Chi-sq	p-val
Allele1 from DBHu2 and u1	37	22	3.81	0.0508
Allele1 from DBHu2 and DBHp444a	45	29	3.46	0.0629
Allele1 from DBHu1 and DBHp444a	43	23	6.06	0.0138
Allele1 from all three SNPs	46	25	6.21	0.0127
Replication/DePaulo				
Allele1 from DBHu2 and u1	18	11	1.69	0.1936
Allele1 from DBHu2 and DBHp444a	32	14	7.04	0.0080
Allele1 from DBHu1 and DBHp444a	31	18	4.79	0.0287
Allele1 from all three SNPs	31	11	9.52	0.0020
Totals				
Allele1 from DBHu2 and u1	55	33	5.50	0.0190
Allele1 from DBHu2 and DBHp444a	77	43	9.63	0.0019
Allele1 from DBHu1 and DBHp444a	74	38	10.84	0.0010
Allele1 from all three SNPs	77	38	14.88	0.0001

FIG. 2